

- 50 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COHEN, CHARLES M.
- (ii) TITLE OF INVENTION: TREATMENT OF MAMMALIAN MYOCARDIUM WITH MORPHOGENICALLY-TREATED MYOGENIC PRECURSOR CELLS
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT, LLP
 - (B) STREET: 125 HIGH STREET
 - (C) CITY: BOSTON
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: TWOMEY, MICHAEL J
 - (B) REGISTRATION NUMBER: 38,349
 - (C) REFERENCE/DOCKET NUMBER: CRP-123
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617/248-7000
 - (B) TELEFAX: 617/248-7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: /label= Generic-Seq-7
/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- 51 -

```

Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
1           5           10           15
Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
           20           25           30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
           35           40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
           50           55           60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
           65           70           75           80
Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
           85           90           95
Xaa

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= Generic-Seq-8
/note= "wherin each Xaa is independently selected
from a group of one or more specified amino acids
as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
1           5           10           15
Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
           20           25           30
Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
           35           40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
           50           55           60
Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
           65           70           75           80
Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
           85           90           95
Xaa Xaa Cys Xaa Cys Xaa
           100

```

- 52 -

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= OPX
 /note= "WHEREIN EACH XAA IS INDEPENDENTLY SELECTED
 FROM A GROUP OF ONE OR MORE SPECIFIED AMINO ACIDS
 AS DEFINED IN THE SPECIFICATION"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Xaa | Xaa | His | Glu | Leu | Tyr | Val | Xaa | Phe | Xaa | Asp | Leu | Gly | Trp | Xaa | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Asp | Trp | Xaa | Ile | Ala | Pro | Xaa | Gly | Tyr | Xaa | Ala | Tyr | Tyr | Cys | Glu | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Glu | Cys | Xaa | Phe | Pro | Leu | Xaa | Ser | Xaa | Met | Asn | Ala | Thr | Asn | His | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ile | Xaa | Gln | Xaa | Leu | Val | His | Xaa | Xaa | Xaa | Pro | Xaa | Xaa | Val | Pro | Lys | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |
| Xaa | Cys | Cys | Ala | Pro | Thr | Xaa | Leu | Xaa | Ala | Xaa | Ser | Val | Leu | Tyr | Xaa | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| Asp | Xaa | Ser | Xaa | Asn | Val | Xaa | Leu | Xaa | Lys | Xaa | Arg | Asn | Met | Val | Val | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Xaa | Ala | Cys | Gly | Cys | His | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 100 |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: HIPPOCAMPUS
- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..139

- 53 -

(D) OTHER INFORMATION: /label= hOP1-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1           5           10           15
Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
          20           25           30
Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
          35           40           45
Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
          50           55           60
Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
          65           70           75           80
Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
          85           90           95
Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
          100          105          110
Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
          115          120          125
Arg Asn Met Val Val Arg Ala Cys Gly Cys His
          130          135

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: /label= MOP1-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1           5           10           15
Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
          20           25           30
Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
          35           40           45

```

- 54 -

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 50 55 60
 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 65 70 75 80
 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 85 90 95
 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 100 105 110
 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 115 120 125
 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 130 135

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS
 - (F) TISSUE TYPE: HIPPOCAMPUS
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..139
 - (D) OTHER INFORMATION: /label= HOP2-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
 1 5 10 15
 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser
 20 25 30
 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
 35 40 45
 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
 50 55 60
 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
 65 70 75 80
 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
 85 90 95
 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
 100 105 110
 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
 115 120 125

- 55 -

Arg Asn Met Val Val Lys Ala Cys Gly Cys His
130 135

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (E) LOCATION: 1..139
- (D) OTHER INFORMATION: /label= MOP2-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu
1 5 10 15
Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
20 25 30
Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg
35 40 45
Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
50 55 60
Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn
65 70 75 80
Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
85 90 95
Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
100 105 110
Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
115 120 125
Arg Asn Met Val Val Lys Ala Cys Gly Cys His
130 135

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 56 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: bovinae

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..101

(D) OTHER INFORMATION: /label= CBMP-2A-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
 20 25 30
 Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
 50 55 60
 Lys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(F) TISSUE TYPE: hippocampus

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..101

(D) OTHER INFORMATION: /label= CBMP-2B-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
 20 25 30
 Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45

- 57 -

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
 50 55 60
 Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DROSOPHILA MELANOGASTER

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: /label= DPP-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
 1 5 10 15
 Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
 20 25 30
 Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
 35 40 45
 Val Val Gln Thr Leu Val Asn Asn Asn Asn Pro Gly Lys Val Pro Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
 65 70 75 80
 Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
 85 90 95
 Val Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 58 -

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: XENOPUS

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= VGL-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
1      5      10      15
Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
20     25     30
Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
35     40     45
Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
50     55     60
Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
65     70     75     80
Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
85     90     95
Asp Glu Cys Gly Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= VGR-1-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Val Gly Trp Gln
1      5      10      15
Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
20     25     30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35     40     45

```

- 59 -

Ile Val Gln Thr Leu Val His Val Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (E) TISSUE TYPE: brain
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (E) LOCATION: 1..106
 - (D) OTHER INFORMATION: /note= "GDF-1 (fx)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His
 1 5 10 15
 Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly
 20 25 30
 Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala
 35 40 45
 Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro Gly
 50 55 60
 Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser
 65 70 75 80
 Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr Glu
 85 90 95
 Asp Met Val Val Asp Glu Cys Gly Cys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids

- 60 -

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1922 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
 (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "OP1"
 /evidence= EXPERIMENTAL
 /standard_name= "OP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG	57
Met His Val	
1	
CGC TCA CTG CBA GGT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
5 10 15	
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
20 25 30 35	
GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
Glu Val His Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
40 45 50	
CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
55 60 65	

- 61 -

CCG CCG CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met 70 75 80	297
CTG GAC CTC TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GCG CCG GCG Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly 85 90 95	345
GGC CAG GGC TTC TCG TAC CCG TAC AAG GCC CTC TTC AGT ACC CAG GGT Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly 100 105 110 115	393
CCC CTT CTC GCC AGC CTC CAA GAT AGC CAT TTC CTC ACC GAC GCG GAC Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp 120 125 130	441
ATG CTC ATG AGC TTC CTC AAC CTC GTG GAA CAT GAC AAG GAA TTC CTC Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe 135 140 145	489
CAC CCA CCG TAC CAC CAT CGA GAG TTC CCG TTT GAT CTT TCG AAG ATC His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile 150 155 160	537
CCA GAA GCG GAA GGT GTC ACG GCA GCC GAA TTC CCG ATC TAC AAG GAC Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp 165 170 175	585
TAC ATC CCG GAA CCG TTC GAC AAT GAG ACG TTC CCG ATC ACC GTT TAT Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr 180 185 190 195	633
CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu 200 205 210	681
GAC AGC GGT ACC CTC TGG GCC TCG GAG GAG GGC TGG TTG GTG TTT GAC Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp 215 220 225	729
ATC ACA GGC ACC AGC AAC CAC TGG GTG GTC AAT CCG CCG CAC AAC CTC Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu 230 235 240	777
GGC CTC CAG CTC TCG GTG GAG ACG CTC GAT GCG CAG AGC ATC AAC CCG Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255	825
AAG TTG GCG GCG CTC ATT GGG CCG CAC GCG CCC CAG AAC AAG CAG CCG Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
TTG ATG GTG CTT TTC TTC AAG GCC ACG GAG GTC CAC TTC CCG AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
CGG TCG AAG GCG AGC AAA CAG CGC ACG CAG AAC CCG TCG AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
AAG AAC CAG GAA GCC CTC CCG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017

- 62 -

AGC GAG CAG AGG CAG GGC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC 1365
 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
 325 330 335
 CGA GAG CTG GGC TGG CAG GAG TGG ATC ATC GCG CCT GAA GGC TAC GCC 1113
 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
 340 345 350 355
 GGC TAA TAC TGT GAG GGG GAG TGT GGC TTC CCT CTG AAC TCC TAC ATG 1161
 Ala Tyr Tyr Cys Glu Gly Gln Cys Ala Phe Pro Leu Asn Ser Tyr Met
 360 365 370
 AAC GGC ACC AAC CAC GGC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC 1209
 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
 375 380 385
 CCG GAA ACG GTG GCG AAG CCG TGC TGT GCG CCC ACG CAG CTC AAT GGC 1257
 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
 390 395 400
 AIC TCC GTC CTC TAC TTC CAT GAG AGC TCC AAC GTC ATC CTG AAG AAA 1305
 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
 405 410 415
 TAC AGA AAC ATG GTC GTC CGC GCC TGT GGC TGC CAC TAGCTCCTCC 1351
 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430
 GAGAATTTCAG ACCCTTGGGG GCGAAGTTTT TTTGGATCCT CCATTGCTCG CCTTGGCCAG 1411
 GAACCAGCAG ACCAACTGCC TTTTGGGAGA CTTTCCCTTC CCTATCCCCA ACTTTAAAGG 1471
 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCASTTTTT CAGTGGCAGC 1531
 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAAAC TAGCAGGAAA AAAAAACAAC 1591
 GCATAAAGAA AAATGGGCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651
 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711
 GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAG GAAAATTGAC CCGGAAGTTC 1771
 CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30

- 63 -

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45
 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

- 64 -

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (E) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMERYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1393
- (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "MOP1"
 /note= "MOP1 (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGCAGCAAG TGACCTGGG TCSTGGACCG CTGCCCTGCC CCCTCCGCTG CCACTG3GGG 60

CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGT 115
 Met His Val Arg
 1

TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT 163
 Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro
 5 10 15 20

CTG TTC TTG CTG CGC TCC GCC CTG GCG GAT TTC AGC CTC GAC AAC GAG 211
 Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu
 25 30 35

GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CCC AGC CAG GAG CGG CGG 259
 Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg
 40 45 50

GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CGG 307
 Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro
 55 60 65

CGC CGG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG 355

- 65 -

Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	Leu		
	70					75					80						
GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	AGC	GGG	CCG	GAC	GGG	CAG	403	
Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Ser	Gly	Pro	Asp	Gly	Gln		
85					90					95					100		
GGG	TTC	TCT	TAC	CCC	TAC	AAG	GCC	CTC	TTC	AGT	ACC	CAG	GGC	CCC	CCG	451	
Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro		
				105					110					115			
TTA	GCC	AGC	CTG	CAG	GAC	AGC	CAT	TTC	CTC	ACT	GAC	GGC	GAC	ATG	CTC	499	
Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val		
			120					125					130				
ATG	AGC	TTC	GTC	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCG	547	
Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro		
	135					140						145					
CGA	TAC	CAC	CAT	CCG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595	
Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu		
150						155					160						
GGC	GAA	CCG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643	
Gly	Glu	Arg	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile		
165					170					175					180		
CGG	GAG	CGA	TTT	GAC	AAC	GAG	ACC	TTC	CAG	ATC	ACA	GTC	TAT	CAG	GTG	691	
Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Gln	Ile	Thr	Val	Tyr	Gln	Val		
				185					190					195			
CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TGG	GAC	CTC	TTC	TTG	CTG	GAC	AGC	739	
Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser		
			200					205					210				
CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GGC	TGG	TTG	GTC	TTT	GAT	ATC	ACA	787	
Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr		
	215						220					225					
GCC	ACC	AGT	AAC	CAC	TGG	GTG	GTC	AAC	CCG	CGG	CAC	AAC	CTG	GGC	TTA	835	
Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu		
230						235					240						
CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GCG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	883	
Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu		
245					250					255					260		
GCA	GGC	CTG	ATT	GGA	CCG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931	
Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met		
				265				270						275			
GTG	GCC	TTC	TTC	AAG	GCC	ACG	GAA	GTC	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979	
Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser		
			280					285					290				
ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027	
Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn		
	295						300					305					
CAA	GAG	GCC	CTG	AGG	ATG	GCC	AGT	GTG	GCA	GAA	AAC	AGT	AGC	AGT	GAC	1075	
Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp		
310						315					320						

- 66 -

CAG AGG CAG CCC TGG AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAG 1123
 Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp
 315 330 335 340
 CTT GGC TGG CAG GAG TGG ATC ATT GCA CCT GAA GGC TAT GCT GGC TAC 1171
 Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr
 345 350 355
 TAC TGT GAG GGA GAG TGG GGC TTC CCT CTG AAC TCC TAC ATG AAC GGC 1219
 Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala
 360 365 370
 ACC AAC CAC GGC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAG 1267
 Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp
 375 380 385
 ACA GTA CCC AAG CCC TGG TGT GCG CCC ACC CAG CTC AAC CCC ATC TCT 1315
 Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
 390 395 400
 GTC CTC TAC TTC GAC GAG AGC TGT AAT CTC ATC CTC AAG AAG TAC AGA 1363
 Val Leu Tyr Phe Asp Asn Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg
 405 410 415 420
 AAC ATG CTG CTC CGC CCC TGT GGC TGC CAC TACCTCTTCC TGAGACCCCTG 1413
 Asn Met Val Val Arg Ala Cys Gly Cys His
 425 430
 ACCTTTGCGG GGGCACACCT TTCCAAATCT TCGATGTCT ACCATCTAAG TCTCTCAGTG 1473
 CCCACCTTGG CAGAGGAGAA AGACCAACCT CTCCTGAGCC TTCCCTEACG TCCCAACCGG 1533
 AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCCGC CTTTCTTTCT 1593
 GGCACGTGAG GGACAAGATC CTACAGCTA CCACAACAAA CGCTTAAGAG CAGGAAAAAT 1653
 GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCTCTGCG GGTCTGAGT TTTGAGGAGT 1713
 AATCGCAAG CTCTTTCAGC TSCAAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCCTGSGCG 1773
 TCTGTGTTGA AGAGAAACCA AGCAGAGGCC ACTGTAATGA TATGTACAA TAAACCCAT 1833
 GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC 1873

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30
 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser

- 67 -

35	40	45
Gln Glu Arg Arg Glu Met	Gln Arg Glu Ile Leu Ser	Ile Leu Gly Leu
50	55	60
Pro His Arg Pro Arg Pro	His Leu Gln Gly Lys	His Asn Ser Ala Pro
65	70	75
Met Phe Met Leu Asp Leu	Tyr Asn Ala Met Ala Val	Glu Glu Ser Gly
85	90	95
Pro Asp Gly Gln Gly Phe	Ser Tyr Pro Tyr Lys Ala	Val Phe Ser Thr
100	105	110
Gln Gly Pro Pro Leu Ala	Ser Leu Gln Asp Ser His	Phe Leu Thr Asp
115	120	125
Ala Asp Met Val Met Ser	Phe Val Asn Leu Val Glu	His Asp Lys Glu
130	135	140
Phe Phe His Pro Arg Tyr	His His Arg Glu Phe Arg	Phe Asp Leu Ser
145	150	155
Lys Ile Pro Glu Gly Glu	Arg Val Thr Ala Ala Glu	Phe Arg Ile Tyr
165	170	175
Lys Asp Tyr Ile Arg Glu	Arg Phe Asp Asn Glu Thr	Phe Gln Ile Thr
180	185	190
Val Tyr Gln Val Leu Gln	Glu His Ser Gly Arg Glu	Ser Asp Leu Phe
195	200	205
Leu Leu Asp Ser Arg Thr	Ile Trp Ala Ser Glu Glu	Gly Trp Leu Val
210	215	220
Phe Asp Ile Thr Ala Thr	Ser Asn His Trp Val Val	Asn Pro Arg His
225	230	235
Asn Leu Gly Leu Gln Leu	Ser Val Glu Thr Leu Asp	Gly Gln Ser Ile
245	250	255
Asn Pro Lys Leu Ala Gly	Leu Ile Gly Arg His Gly	Pro Gln Asn Lys
260	265	270
Gln Pro Phe Met Val Ala	Phe Phe Lys Ala Thr Glu	Val His Leu Arg
275	280	285
Ser Ile Arg Ser Thr Gly	Gly Lys Gln Arg Ser Gln	Asn Arg Ser Lys
290	295	300
Thr Pro Lys Asn Gln Glu	Ala Leu Arg Met Ala Ser	Val Ala Glu Asn
305	310	315
Ser Ser Ser Asp Gln Arg	Gln Ala Cys Lys Lys His	Glu Leu Tyr Val
325	330	335
Ser Phe Arg Asp Leu Gly	Trp Gln Asp Trp Ile Ile	Ala Pro Glu Gly
340	345	350
Tyr Ala Ala Tyr Tyr Cys	Glu Gly Glu Cys Ala Phe	Pro Leu Asn Ser
355	360	365
Tyr Met Asn Ala Thr Asn	His Ala Ile Val Gln Thr	Leu Val His Phe

- 68 -

370 375 380
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 490..1696
- (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "hOP2-PP"
 /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGC3CCGG3CA BAC3AGGAGT G3CT3GAGGA GCTGTG3TT3 GAGCAGGAGG TBGCACG3CA 60
 GGGGT3GAGG BCTCCCTAT3 AGT3GCGGAG ACG3CCAG3 AGGCGCTGGA GCAACAG3TC 120
 CCACA3CGCA CCAAGCGGT3 GCTGCAGGAG CTG3CCCAT3 G3CCCTGCG3 TGCTCGGACC 180
 GCGGCCACAG CCGGACTGG3 GGGTACGGG3 GCGACAGAG3 CATTTGGCCGA GAGTCCCAST 240
 CG3CAGAGTA G3CC3GGCT CGAG3CGGTG G3TCCCGGT CTTCTCCCT3 CAGGAG3CA3 300
 GACAGGTGTC G3GCG3CGG3 GCTCCAGGGA CC3G3CCTGA G3CCGGGTG3 C3G3CG3TC 360
 CGCC3CGGCC C3CG3CC3GC CGCCCGCCGA G3CCAGCCT3 CTTGCCGTG3 G3GCGTCCCC 420
 AG3C3CTGGG TGG3CGG3 AGCCSATGCG C3CC3CTGA G3CC3CCAG3 TBAGC3CCCC 480
 CG3CCTGCC AT3 ACC G3G CTC CCC G3G CCG CTC TGG CTC CTG G3G CTC 528
 Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu
 1 5 10
 G3G CTA TGC GCG CTC GGC G3G G3G G3G CCC G3G CTC CGA C3G CCG CCG 576
 Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro
 15 20 25
 G3G TGT CCC CAG CGA CGT CTG G3G G3G CCG GAG CCG CCG GAC CTG CAG 624
 Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Gln Arg Arg Asp Val Gln
 30 35 40 45

CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCG GGC	672
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
50 55 60	
GCG CCA CCC GCG GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
65 70 75	
CTG GAC CTG TAC CAC GGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG	768
Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
80 85 90	
CCC GCG GAG GCG CGC CTG GCG GCG GCG GAC CTG GTC ATG ATC TTC ATT	816
Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
95 100 105	
AAC ATG GTG GAG CGA GAC CCG GCG CTG GCG CAC TAG GAG CTC CAT TGG	864
Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
110 115 120 125	
AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GCG GAG GCG CTC	912
Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
130 135 140	
ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
145 150 155	
AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG CTC CAG GAG CAG TCC	1008
Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	
160 165 170	
AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACC CTC CGA GGT	1056
Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala	
175 180 185	
GGA GAC GAG GCG TGG CTG GTG CTG GAT GTC ACA GCA GCG AGT GAC TGC	1104
Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys	
190 195 200 205	
TGG TTG CTG AAG CCG CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG	1152
Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu	
210 215 220	
ACT GAG GAC GCG CAC AGC GTG GAT CCT GGC CTG GCC GCG CTC CTG GGT	1200
Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly	
225 230 235	
CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG	1248
Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg	
240 245 250	
GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG	1296
Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg	
255 260 265	
AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCG AAC CCA CTC	1344
Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu	
270 275 280 285	
CCA GCG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CCG CAG GTC TCC	1392
Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys	
290 295 300	

- 70 -

CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC 1440
 Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp
 305 310 315

TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG 1488
 Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu
 320 325 330

TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCG ACC AAC CAC GCC ATC 1536
 Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile
 335 340 345

CTG CAG TCC CTG GTG CAG CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG 1584
 Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala
 350 355 360 365

TGC TGT GCA CCC ACC AAG CTG AGC GCG ACC TCT GTG CTC TAC TAT GAC 1632
 Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
 370 375 380

AGC AGC AAC AAC CTC ATC CTG CGT AAA CAG CGC AAC ATG GTG GTC AAG 1680
 Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys
 385 390 395

GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG 1723
 Ala Cys Gly Cys His
 400

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15

Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
 20 25 30

Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
 35 40 45

Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
 50 55 60

Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
 65 70 75 80

Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
 85 90 95

Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
 100 105 110

Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe

- 71 -

115	120	125
Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala		
130	135	140
Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr		
145	150	155
Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu		
165	170	175
Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu		
180	185	190
Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu		
195	200	205
Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp		
210	215	220
Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala		
225	230	235
Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro		
245	250	255
Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln		
260	265	270
Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile		
275	280	285
Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His		
290	295	300
Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile		
305	310	315
Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe		
325	330	335
Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser		
340	345	350
Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala		
355	360	365
Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn		
370	375	380
Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly		
385	390	395
		400
Cys His		

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1926 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 72 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MURIDAE
(F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 93..1289
(D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "mOP1-pp"
/note= "MOI2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

GCCAGATACA GGTGCGCTGT CTGGTCTCTC CCGTCTGCGG TCAGCCGAGT CCGACCAGCT      60
ACCAATGAGAT GGCGGTGGGG TGAAAGTCCG AG ATG GCT ATG CGT CCC GGG CCA      113
                                     Met Ala Met Arg Pro Gly Pro
                                     1           5
CTC TGG CTA TTG GGC GTT GCT CTC TGC GCG CTG GGA GGC GGC CAC GCT      161
Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly Gly His Gly
          10          15          20
CCG CGT CCC CCC TAC ACC TGT CCC CAG CGT GCG CTC GGA GCG CGC CAG      209
Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu
          25          30          35
CGC CGC GAG ATG CAG CGT GAA ATC CTC GCG CTC CTC GGC CTA CCC GGA      257
Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly
          40          45          50          55
CGG CCT CGA CCC CGT GCA CAA CCC GCG GCT GCG CGG CAG CCA GCG TCC      305
Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln Pro Ala Ser
          60          65          70
GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC GAT GAC GAC      353
Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr Asp Asp
          75          80          85
GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC CTC GTC ATG      401
Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp Leu Val Met
          90          95          100
AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTC GGC TAC CAG GAG      449
Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly Tyr Gln Glu
          105          110          115
CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC CCT GCT GGG      497
Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile Pro Ala Gly
          120          125          130          135
GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC AGC ACC      545
Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro Ser Thr
          140          145          150
CAC CGG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA GTG GTC CAA      593
His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu Val Val Gln
          155          160          165
GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACC      641
Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr

```

- 73 -

170	175	180	
CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTC GAC ATC ACA GCA GCG Leu Arg Ser Gly Asp Gln Gly Trp Leu Val Leu Asp Ile Thr Ala Ala 185 190 195			689
AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA CTC GGC CTC Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly Leu Arg Leu 200 205 210 215			737
TAT GTG GAA AGC GGG GAT GGG CAC ACC ATG CAT CCT GGC CTG GCT GGT Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly Leu Ala Gly 220 225 230			785
CTG CTT GGA CGA CAA GCA CCA GGC TCC ASA CAG CCT TTC ATG GTA ACC Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe Met Val Thr 235 240 245			833
TTC TTC AGG GGC AGC CAG AGT CCT GTG GGG GGC CCT CGG GCA GCG AGA Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg Ala Ala Arg 250 255 260			881
CCA CTG AAG AGG AGG CAG CCA AAG AAA AGC AAC GAG CTT CGG CAC CCC Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu Pro His Pro 265 270 275			929
AAC AAA CTC GCA GGG ATC TTT GAT GAT GGC CAC GGT TCC CGG GGC AGA Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly Arg 280 285 290 295			977
GAG GTT TGC GGC AGG CAT GAG CTC TAC GTC ACC TTC CBT GAC CTT GGC Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly 300 305 310			1025
TGG CTG GAT TGG GTC ATC GCC CCC CAG GGC TAC TCT GGC TAT TAC TGT Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys 315 320 325			1073
GAG GGG GAG TGT GGT TTC CCA CTG GAC TCC TGT ATG AAC GGC ACC AAC Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn 330 335 340			1121
CAT GGC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT GTC His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val Val 345 350 355			1169
CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GGC ACC TCT GTG CTG Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu 360 365 370 375			1217
TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CBT AAA CAC CGT AAC ATG Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met 380 385 390			1265
GTG GTC AAG GGC TGT GGC TGC CAC TTAGGCGCG CCCAGCATCC TCCTTCTACT Val Val Lys Ala Cys Gly Cys His 395			1319
ACCTTACCAT CTGGCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT TATCATAGCT			1379
CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCCTGCTA AAATTCTGGT			1439
CTTCCCACT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCAGCCCGGC CTCTCCATCC			1499

- 74 -

TCTTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA ACTGAGAGGT 1559
 CTGGGGSTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGSCCATE CTCAGGCCAC 1619
 AATGGGAAAT TCTGGATGCT TTAAGAAGGC CCTGGAATTC TAAACTAGAT GATCTGGGCT 1679
 CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTITAGGT ATAACAGACA CATACATTTA 1739
 GATCAATGCA TGGGTGTACT CTTTGAAATC AGACCTAGCT TGTTAGAAAA AGAATCAGAG 1799
 CCAGSTATAG CGGTGCATGT CATTAATGTC AGCCTAAAG AGACAGAGAC AGGAGAATCT 1859
 CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTGGGGA GCAGGAAAAA AAAAAAAAC 1919
 GGAATTC 1926

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- A) LENGTH: 399 amino acids
- B) TYPE: amino acid
- C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15
 Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln
 20 25 30
 Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu
 35 40 45
 Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala
 50 55 60
 Ala Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr
 65 70 75 80
 His Ala Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu
 85 90 95
 Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp
 100 105 110
 Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp
 115 120 125
 Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg
 130 135 140
 Ile Tyr Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile
 145 150 155 160
 Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu
 165 170 175
 Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu

- 75 -

180	185	190
Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His 195 200 205		
Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser 210 215 220		
Met Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser 225 230 235 240		
Arg Gln Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val 245 250 255		
Arg Ala Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys 260 265 270		
Thr Asn Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp 275 280 285		
Gly His Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr 290 295 300		
Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln 305 310 315 320		
Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp 325 330 335		
Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His 340 345 350		
Leu Met Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys 355 360 365		
Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile 370 375 380		
Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His 385 390 395		

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368
- (D) OTHER INFORMATION: /label= "60A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC
Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
1 5 10 15

- 76 -

CTG GGA CTC GGA ATG BTT CTG CTC ATG TTC GTG GGG ACC AAG CCG CTG Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	96
20 25 30	
GCC BTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	144
35 40 45	
CAG AAG ATC ATG CAC AGA GTG CTG AAC GAG GAC GAC AAG CTG GAC CTC Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Lys Leu Asp Val	192
50 55 60	
TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GTC GAA CCG GCG ACG CAC Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	240
65 70 75 80	
CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCG AAG TTC CTG Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	288
85 90 95	
CTG GAC CTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC ACC GAT CAG Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln	336
100 105 110	
GAT GAG GAC GAC GAC TAC GAA CGC GGT CAT CCG TCC AGG AGG ACC GCC Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala	384
115 120 125	
GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATC ACC GAC Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp	432
130 135 140	
CTG GAC AAG CCG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu	480
145 150 155 160	
AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg	528
165 170 175	
CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val	576
180 185 190	
ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu	624
195 200 205	
ATC GCC AAC AGG GAG TTC ACC ATC ACG GTA TAC GCC ATT GGC ACC GGC Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly	672
210 215 220	
ACG CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr	720
225 230 235 240	
GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His	768
245 250 255	
GAG TGG CTG GTC AAG TGG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala	816

- 77 -

260	265	270	
CAC GGT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC CAC ATT GGA His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly 275 280 285			864
CTG ATC CAC CAC AAG CTC GAC GAG GAG TTC CAG CCC TTC ATG ATC GGC Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly 290 295 300			912
TTC TTC CCC GGA CCG GAG CTG ATT AAG GCG ACG GGC CAC AGC AGC CAC Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His 305 310 315 320			960
CAC AGC AGC AAG CGA AGC CCC AGC CAT CCA CGC AAG CGC AAG AAG TCG His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser 325 330 335			1008
GTG TCG CCC AAC AAC CTG CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg 340 345 350			1056
AGC TGT CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp 355 360 365			1104
CAT GAG TGG ATC ATC GCA CCA GAG GGC TAT GGC GGC TTC TAC TGC AGC His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser 370 375 380			1152
GGC GAG TGC AAT TTC CCG CTC AAT GCG CAC ATG AAC GGC ACG AAC CAT Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His 385 390 395 400			1200
GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAG GTG CCC Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro 405 410 415			1248
AAG CCG TGC TGC GGT CCG ACC AGG CTG GGA GGA CTA CCG GTT CTG TAC Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr 420 425 430			1296
CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile 435 440 445			1344
GTG AAA TCC TGC GGG TGC CAT TGA Val Lys Ser Cys Gly Cys His 450 455			1368

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser

- 78 -

1	5	10	15
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	20	25	30
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	35	40	45
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	50	55	60
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	65	70	75
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	85	90	95
Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln	100	105	110
Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala	115	120	125
Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp	130	135	140
Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu	145	150	155
Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg	165	170	175
Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val	180	185	190
Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu	195	200	205
Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly	210	215	220
Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr	225	230	235
Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His	245	250	255
Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala	260	265	270
His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly	275	280	285
Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly	290	295	300
Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His	305	310	315
His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser	325	330	335
Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg			

- 79 -

340	345	350
Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp		
355	360	365
His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser		
370	375	380
Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His		
385	390	395
Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro		
405	410	415
Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr		
420	425	430
His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile		
435	440	445
Val Lys Ser Cys Gly Cys His		
450	455	

(2) INFORMATION FOR SEQ ID NO:25:

- i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (E) LOCATION: 69..1268
- (D) OTHER INFORMATION: /note= "mDP3-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCCGCGG CGCTGTCCCA TCCTTGTCGT CGAGGCGTCG CTGGATGCGA GTCCGCTAAA	60
CGTCCGAG ATG GCT GCG CGT CCG GGA CTC CTA TGG CTA CTG GGC CTG GGT	110
Met Ala Ala Arg Pro Gly Leu Leu Trp Leu Leu Gly Leu Ala	
1 5 10	
CTG TGC GTG TTG GGC GGC GGT CAC CTC TCG CAT CCC CCG CAC GTC TTT	158
Leu Cys Val Leu Gly Gly Gly His Leu Ser His Pro Pro His Val Phe	
15 20 25 30	
CCC CAG CGT CGA CTA GGA GTA GGC GAG CCC GGC GAC ATG CAG CGC GAG	206
Pro Gln Arg Arg Leu Gly Val Arg Glu Pro Arg Asp Met Gln Arg Glu	
35 40 45	
ATT CGG GAG GTG CTG GGG CTA GGC GGG CGG CCC CGA TCC CGA GCA CCG	254
Ile Arg Glu Val Leu Gly Leu Ala Gly Arg Pro Arg Ser Arg Ala Pro	
50 55 60	
GTC GGG GCT GCC CAG CAG CCA GCG TCT GCG CCC CTC TTT ATG TTG GAC	302
Val Gly Ala Ala Gln Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp	

- 80 -

65	70	75	
CTG TAC CCG GCC ATG ACG GAT GAC AGT GGC GGT GGG ACC CCG CAG CCT Leu Tyr Arg Ala Met Thr Asp Asp Ser Gly Gly Gly Thr Pro Gln Pro 80 85 90			350
CAC TTG GAG CCG GCT GAC CTG ATT ATG ACG TTT GTC AAC ATA GTG GAA His Leu Asp Arg Ala Asp Leu Ile Met Ser Phe Val Asn Ile Val Glu 95 100 105 110			398
CGC GAC CCG ACC CTG GGC TAC CAG GAG CCA CAC TGG AAG GAA TTC TAC Arg Asp Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His 115 120 125			446
TTT GAC CTA ACC CAG ATC CCG GCT GGG GAG GGT GTC ACA GGT GGT GAG Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu 130 135 140			494
TTC CGG ATC TAC AAA GAA CCC AGT ACC CAC CCG CTC AAC ACA ACC CTC Phe Arg Ile Tyr Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu 145 150 155			542
CAC ATC AGC ATG TTC GAA GTG CTC CAA GAG CAC TCC AAC ACG GAG TCT His Ile Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser 160 165 170			590
GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA TTT GGG GAG GAG GGC Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly 175 180 185 190			638
TGG CTG GTG CTG GAC ATC ACA GCA CCC AGT GAC CGA TGG CTG CTG AAC Trp Leu Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn 195 200 205			686
CAT CAC AAG GAC CTA GGA CTC CGC CTC TAT GTG GAA ACC GAG GAT GGG His His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly 210 215 220			734
CAC AGC ATA GAT CCG GGC CTA GGT GGT CTG CTT GGA CGA CAA GCA CCA His Ser Ile Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro 225 230 235			782
CGC TCC AGA CAG CCG TTC ATG GTT GGT TTC TTC ACG GCC AAC CAG AGT Arg Ser Arg Gln Pro Phe Met Val Gly Phe Phe Arg Ala Asn Gln Ser 240 245 250			830
CCT GTG CGG GCC CCG CGA ACA GCA AGA CCA CTG AAG AAG AAG CAG CTA Pro Val Arg Ala Pro Arg Thr Ala Arg Pro Leu Lys Lys Lys Gln Leu 255 260 265 270			878
AAT CAA ATC AAC CAG CTG CCG CAC TCC AAC AAA CAC CTA GGA ATC CTT Asn Gln Ile Asn Gln Leu Pro His Ser Asn Lys His Leu Gly Ile Leu 275 280 285			926
GAT GAT GGC CAC GGT TCT CAC GGC AGA GAA GTT TGC CGC ACG CAT GAG Asp Asp Gly His Gly Ser His Gly Arg Glu Val Cys Arg Arg His Glu 290 295 300			974
CTC TAT GTC AGC TTC CCG GAC CTT GGC TGG CTG GAC TCT GTC ATT GGC Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Ser Val Ile Ala 305 310 315			1022
CCC CAG GGC TAC TCC GCC TAT TAC TGT GGT GGG GAG TGC ATC TAC CCA			1070

- 81 -

Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Ala Gly Glu Cys Ile Tyr Pro
 320 325 330

CTG AAC TCC TGT ATG AAC TCC ACC AAC CAC GCC ACT ATG CAG GCC CTG 1118
 Leu Asn Ser Cys Met Asn Ser Thr Asn His Ala Thr Met Gln Ala Leu
 335 340 345 350

GTA CAT CTG ATG AAG CCA GAT ATC ATC CCC AAG GTG TGC TGT GTG CCT 1166
 Val His Leu Met Lys Pro Asp Ile Ile Pro Lys Val Cys Cys Val Pro
 355 360 365

ACT GAG CTG AGT GCC ATT TCT CTG CTC TAC TAT GAT AGA AAC AAT AAT 1214
 Thr Gln Leu Ser Ala Ile Ser Leu Leu Tyr Tyr Asp Arg Asn Asn Asn
 370 375 380

GTC ATC CTG CGC AGG GAG CGC AAC ATG GTA GTC CAG GCC TGT GGC TGC 1262
 Val Ile Leu Arg Arg Glu Arg Asn Met Val Val Gln Ala Cys Gly Cys
 385 390 395

CAC TGAGTCCCTG CCCAACAGCC TCCTGCCATC CCATCTATCT AGTCAGGCCT 1315
 His
 400

CTCTTCCAAAG GCAGGAAACC AACAAAGAGG GAAAGCAATG CTTTCAACTC CATGTCCACA 1375

TTCACASTCT TGGCCCTCTC TGTTCTTTTT GCCAAGGCTG AGAAGATGGT CCTAGTIATA 1435

ACCCTGSTGA CCTCAGTAGC CCGATCTCTC ATCTCCCAAA ACTCCCAAT GCAGCCAGGG 1495

GCATCTATGT CTTTGGGAT TGGGCACAGA AGTCCAATTT ACCAAETTAT TCATGASTCA 1555

CTACTGCCCC AAGCTGACT TGAACCTGGA ACACAGGGTA GAGTCAGGC TCTTCAGTAT 1615

CCATCAGAAG ATTTAGGTGT GTGCAGACAT GACCACACTC CCCCTAGCAC TCCATAGCC 1674

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Ala Arg Pro Gly Leu Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15

Val Leu Gly Gly Gly His Leu Ser His Pro Pro His Val Phe Pro Gln
 20 25 30

Arg Arg Leu Gly Val Arg Glu Pro Arg Asp Met Gln Arg Glu Ile Arg
 35 40 45

Glu Val Leu Gly Leu Ala Gly Arg Pro Arg Ser Arg Ala Pro Val Gly
 50 55 60

Ala Ala Gln Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr
 65 70 75 80

Arg Ala Met Thr Asp Asp Ser Gly Gly Gly Thr Pro Gln Pro His Leu

- 82 -

85	90	95
Asp Arg Ala Asp Leu Ile Met Ser Phe Val Asn Ile Val Glu Arg Asp 100 105 110		
Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp 115 120 125		
Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg 130 135 140		
Ile Tyr Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile 145 150 155 160		
Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu 165 170 175		
Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu 180 185 190		
Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His 195 200 205		
Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser 210 215 220		
Ile Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser 225 230 235 240		
Arg Gln Pro Phe Met Val Gly Phe Phe Arg Ala Asn Gln Ser Pro Val 245 250 255		
Arg Ala Pro Arg Thr Ala Arg Pro Leu Lys Lys Lys Gln Leu Asn Gln 260 265 270		
Ile Asn Gln Leu Pro His Ser Asn Lys His Leu Gly Ile Leu Asp Asp 275 280 285		
Gly His Gly Ser His Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr 290 295 300		
Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Ser Val Ile Ala Pro Gln 305 310 315 320		
Gly Tyr Ser Ala Tyr Tyr Cys Ala Gly Glu Cys Ile Tyr Pro Leu Asn 325 330 335		
Ser Cys Met Asn Ser Thr Asn His Ala Thr Met Gln Ala Leu Val His 340 345 350		
Leu Met Lys Pro Asp Ile Ile Pro Lys Val Cys Cys Val Pro Thr Glu 355 360 365		
Leu Ser Ala Ile Ser Leu Leu Tyr Tyr Asp Arg Asn Asn Asn Val Ile 370 375 380		
Leu Arg Arg Glu Arg Asn Met Val Val Gln Ala Cys Gly Cys His 385 390 395		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 83 -

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note= "BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1           5           10           15
Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
20           25           30
Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35           40           45
Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
50           55           60
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
65           70           75           80
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
85           90           95
Thr Val Glu Ser Cys Ala Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1           5           10           15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20           25           30

```

- 84 -

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid

- 85 -

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS
(F) TISSUE TYPE: BRAIN

(ix) FEATURE:

(A) NAME/KEY: SIS
(B) LOCATION: 84..1199
(C) OTHER INFORMATION: /product= "SDF-1"
/note= "SDF-1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GGGGACACCG GGTCCGGCCCT CAGCCCACTG GTCTCGGGCC GCCGCGGACC CTGCCCACCTC      60
TCTGTCATC GCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC      110
           Met Pro Pro Pro Gln Gln Gly Pro Cys
           1                     5

GGC CAC CAC CTC CTC CTC CTC CTC GGC CTG CTG CTG CCC TGG CTG CCC      158
Gly His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro
10                     15                     20                     25

CTG ACC CSC CCC CCC GTG CCC CCA GGC CCA GGC GCC GCC CTG CTC CAG      206
Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu Gln
           30                     35                     40

GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GGC CCC AGG CTC CGG CCG      254
Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu Arg Pro
           45                     50                     55

GTT CCC CCG CTC ATG TGG CGC CTG TTT CGA CGT CGG GAC CCC CAG GAG      302
Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp Pro Gln Glu
           60                     65                     70

ACC AGG TCT GGC TCG CGG CCG ACC TCT CCA GGG GTC ACC CTG CAA CCG      350
Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val Thr Leu Gln Pro
           75                     80                     85

TGC CAC GTG GAG GAG CTC GGG GTC GGC GGA AAC ATC GTG CGC CAC ATC      398
Cys His Val Glu Glu Leu Gly Val Ala Gly Asn Ile Val Arg His Ile
           90                     95                     100                     105

CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG GAG CCT GTC TCG GCC GCG      446
Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser Glu Pro Val Ser Ala Ala
           110                     115                     120

GGG CAT TGC CCT GAG TGG ACA GTG GTC TTC GAG CTG TCG GCT GTG GAA      494
Gly His Cys Pro Glu Trp Thr Val Val Phe Asp Leu Ser Ala Val Glu
           125                     130                     135

CCC GCT GAG GGC CCG AGC CCG GGC CCG CTG GAG CTG CCT TTC GCG GCG      542
Pro Ala Glu Arg Pro Ser Arg Ala Arg Leu Glu Leu Arg Phe Ala Ala
           140                     145                     150

GGG GCG GCG GGA GGC CCG GAG GGC GGC TGG GAG CTG AGC GTG GCG CAA      590
Ala Ala Ala Ala Ala Pro Glu Gly Gly Trp Glu Leu Ser Val Ala Gln
           155                     160                     165

```

- 86 -

GCG GGC CAG GGC GCG GGC GGC GAC CCC GGG CCG GTG GTG CTC CCG CAG Ala Gly Gln Gly Ala Gly Ala Asp Pro Gly Pro Val Leu Leu Arg Gln 170 175 180 185	638
TTG GTG CCG GGC CTG GGG CCG CCA GTG CCG GAG GAG CTG CTG GAG GGC Leu Val Pro Ala Leu Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala 190 195 200	686
GCT TGG GCT CCG AAC GCG TCA TGG CCG CCG AGC CTC CCG CTG GCG CTG Ala Trp Ala Arg Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu 205 210 215	734
GCG CTA CCG CCG CCG GCG CCG GCG GCG TCG GCG CCG CTG GCG GAG GCG Ala Leu Arg Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala 210 215 220	782
TGG CTG CTG CTG GTG AGC CTC GAC CCG CCG CTG TCG CAG CCG CTG GCG Ser Leu Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala 235 240 245	830
CGG CCG CCG CCG GAC CCG GAA CCG GTG TTG GCG GCG GCG CCG GCG GCG Arg Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly 250 255 260 265	878
GCT TGT CCG GCG CCG CCG CTG TAC GTG AGC TTC CCG GAG GTG GCG TGG Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp 270 275 280	926
CAC CCG TGG GTG ATC GCG CCG CCG GCG TTG TTG GCG AAC TAC TCG CAG His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln 285 290 295	974
GGT CAG TGG GCG CTG CCG GTC GCG CTG TCG GCG TCG GCG GCG CCG CCG Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro 300 305 310	1022
GCG CTC AAC CAC GCT GTG CTG CCG GCG CTC ATG CAC GCG GCG GCG CCG Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro 315 320 325	1070
GGA GCC GCG GAC CTG CCG TGC TGG GTG CCG GCG CCG CTG TCG CCG ATC Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile 330 335 340 345	1118
TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC GTG GTG CTG CCG CAG TAT Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr 350 355 360	1166
GAG GAC ATG GTG GTG GAC GAG TGC GCG TGC CCG TAA CCG GCG CCG GCG Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg 365 370	1219
CCCGGGCCCCA ACAATAAATG CCGCGTGG	1247

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- 87 -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Pro Pro Pro Gln Gln Gly Pro Cys Gly His His Leu Leu Leu Leu
 1 5 10 15
 Leu Ala Leu Leu Leu Pro Ser Leu Pro Leu Thr Arg Ala Pro Val Pro
 20 25 30
 Pro Gly Pro Ala Ala Ala Leu Leu Gln Ala Leu Gly Leu Arg Asp Glu
 35 40 45
 Pro Gln Gly Ala Pro Arg Leu Arg Pro Val Pro Pro Val Met Trp Arg
 50 55 60
 Leu Phe Arg Arg Arg Asp Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg
 65 70 75 80
 Thr Ser Pro Gly Val Thr Leu Gln Pro Cys His Val Glu Glu Leu Gly
 85 90 95
 Val Ala Gly Asn Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr
 100 105 110
 Arg Ala Ser Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr
 115 120 125
 Val Val Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg
 130 135 140
 Ala Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu
 145 150 155 160
 Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly Ala
 165 170 175
 Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu Gly Pro
 180 185 190
 Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg Asn Ala Ser
 195 200 205
 Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg Pro Arg Ala Pro
 210 215 220
 Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu Leu Val Thr Leu
 225 230 235 240
 Asp Pro Arg Leu Cys His Pro Leu Ala Arg Pro Arg Arg Asp Ala Glu
 245 250 255
 Pro Val Leu Gly Gly Gly Pro Gly Gly Ala Cys Arg Ala Arg Arg Leu
 260 265 270
 Tyr Val Ser Phe Arg Glu Val Gly Trp His Arg Trp Val Ile Ala Pro
 275 280 285
 Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly Gln Cys Ala Leu Pro Val
 290 295 300
 Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala Leu Asn His Ala Val Leu
 305 310 315 320

- 88 -

Arg Ala Leu Met His Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys
325 330
Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn
340 345 350
Ser Asp Asn Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu
355 360 365
Cys Gly Cys Arg
370